WEST Search History

DATE: Monday, August 11, 2003

Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT,PGPB,JPAB,EPAB,DWPI; PLUR=YES; OP=OR			
L10	6492117.pn.	2	L10
L9	L8 and (zinc adj2 finger adj2 protein or zfp)	25	L9
L8	L7 and (ATF or artificial adj2 transcription adj2 factor)	182	L8
L7	combinatorial adj3 library	9288	L7
L6	L5 and 256 adj4 bp	6	L6
L5	L4 and zinc adj3 fingers	825	L5
L4	L3 and combinatorial adj3 library	7709	L4
L3	transcription ajd4 factor or tf	916898	L3
DB=USPT; PLUR=YES; OP=OR			
L2	5198346.pn.	1	L2
L1	5198346	173	L1

END OF SEARCH HISTORY

Cambridge, MA, 02139, USA
SO Science (Washington, D. C.) (1997), 275(5300), 657-661
CODEN: SCIEAS; ISSN: 0036-8075
PB American Association for the Advancement of Science
DT Journal
LA English

L3 ANSWER 7 OF 12 CA COPYRIGHT 2003 ACS on STN
AN 123:51506 CA
TI Surface plasmon resonance based kinetic studies of zinc finger-DNA interactions
AU Yang, Wei-Ping; Wu, Herren; Barbas, Carlos F. III
CS Department of Molecular Biology, The Scripps Research Institute, 10666 North Torrey Pines Road, La Jolla, 92037, USA
SO Journal of Immunological Methods (1995), 183(1), 175-82
CODEN: JIMMBG; ISSN: 0022-1759
PB Elsevier
DT Journal
LA English

L3 ANSWER 8 OF 12 CA COPYRIGHT 2003 ACS on STN
AN 122:47734 CA
TI Selection of DNA binding sites for zinc fingers using rationally randomized DNA reveals coded interactions
AU Choo, Yen; Klug, Aaron
CS Med. Res. Counc., Lab. Mol. Biol., Cambridge, CB2 2QH, UK
SO Proceedings of the National Academy of Sciences of the United States of America (1994), 91(23), 11168-72
CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English

L3 ANSWER 9 OF 12 CA COPYRIGHT 2003 ACS on STN
AN 122:47732 CA
TI Length-encoded multiplex binding site determination: application to zinc finger proteins
AU Desjarlais, John R.; Berg, Jeremy M.
CS Thomas C. Jenkins Dep. Biophys., The Johns Hopkins Univ., Baltimore, MD, 21218, USA
SO Proceedings of the National Academy of Sciences of the United States of America (1994), 91(23), 11099-103
CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English

L3 ANSWER 10 OF 12 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
AN 2000:347005 BIOSIS
DN PREV200000347005
TI Regulation of the MDR1 gene by transcriptional repressors selected using peptide **combinatorial libraries**.
AU Bartsevich, Victor V.; Juliano, R. L. (1)
CS (1) Department of Pharmacology, School of Medicine, University of North Carolina, 1106 Jones Bldg., Chapel Hill, NC, 27599-7365 USA
SO Molecular Pharmacology, (July, 2000) Vol. 58, No. 1, pp. 1-10. print.
ISSN: 0026-895X.
DT Article
LA English
SL English

L3 ANSWER 11 OF 12 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
AN 1995:34475 BIOSIS
DN PREV199598048775
TI Length-encoded multiplex binding site determination: Application to zinc

finger proteins.
AU Desjarlais, John R.; Berg, Jeremy M. (1)
CS (1) Thomas C. Jenkins Dep. Biophysics, Johns Hopkins University, Baltimore, MD 21218 USA
SO Proceedings of the National Academy of Sciences of the United States of America, (1994) Vol. 91, No. 23, pp. 11099-11103.
ISSN: 0027-8424.
DT Article
LA English

L3 ANSWER 12 OF 12 MEDLINE on STN
AN 95062213 MEDLINE
DN 95062213 PubMed ID: 7972017
TI Length-encoded multiplex binding site determination: application to zinc finger proteins.
AU Desjarlais J R; Berg J M
CS Thomas C. Jenkins Department of Biophysics, Johns Hopkins University, Baltimore, MD 21218.
SO PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1994 Nov 8) 91 (23) 11099-103.
Journal code: 7505876. ISSN: 0027-8424.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199412
ED Entered STN: 19950110
Last Updated on STN: 19950110
Entered Medline: 19941212

=> d l3 1-12 ab

L3 ANSWER 1 OF 12 CA COPYRIGHT 2003 ACS on STN
AB The present invention provides mol. targets that regulate erythropoiesis. Groups of genes or their encoded gene products comprise panels of the invention and may be used in therapeutic intervention, therapeutic agent screening, and in diagnostic methods for diseases and/or disorders of erythropoiesis. The panels were discovered using gene expression profiling of erythroid progenitors with Affymetrix HU6800 and HG-U95Av2 chips. Cells from an in vitro growth and differentiation system of SCF-Epo dependent human erythroid progenitors, E-cadherin+/CD36+ progenitors, cord blood, or CD34+ peripheral blood stem cells were analyzed. The HU6800 chip contains probes from 13,000 genes with a potential role in cell growth, proliferation, and differentiation and the HG-U95Av2 chip contains 12,000 full-length, functionally-characterized genes. [This abstr. record is one of two records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

L3 ANSWER 2 OF 12 CA COPYRIGHT 2003 ACS on STN
AB The present invention provides mol. targets that regulate erythropoiesis. Groups of genes or their encoded gene products comprise panels of the invention and may be used in therapeutic intervention, therapeutic agent screening, and in diagnostic methods for diseases and/or disorders of erythropoiesis. The panels were discovered using gene expression profiling of erythroid progenitors with Affymetrix HU6800 and HG-U95Av2 chips. Cells from an in vitro growth and differentiation system of SCF-Epo dependent human erythroid progenitors, E-cadherin+/CD36+ progenitors, cord blood, or CD34+ peripheral blood stem cells were analyzed. The HU6800 chip contains probes from 13,000 genes with a potential role in cell growth, proliferation, and differentiation and the HG-U95Av2 chip contains 12,000 full-length, functionally-characterized genes. This abstr. record is one of two records for this document necessitated by the large no. of index entries required to fully index the

document and publication system constraints.

L3 ANSWER 3 OF 12 CA COPYRIGHT 2003 ACS on STN
AB The present invention relates to DNA binding proteins comprising zinc finger domains in which two histidine and two cysteine residues coordinate a central zinc ion. More particularly, the invention relates to the identification of a context-independent recognition code to design zinc finger domains. This code permits identification of an amino acid for positions -1, 2, 3 and 6 of the .alpha.-helical region of the zinc finger domain from four-base pair nucleotide target sequences. The invention includes zinc finger proteins (ZFPs) designed using this recognition code, nucleic acids encoding these ZFPs and methods of using such ZFPs to modulate gene expression, alter genome structure, inhibit viral replication and detect alterations (e.g., nucleotide substitutions, deletions or insertions) in the binding sites for such proteins. In addn., the invention provides a rapid method of assembling a **ZFP** with three or more zinc finger domains using three sets of 256 oligonucleotides, where each set is designed to target the 256 different 4-base pair targets and allow prodn. of all possible 3-finger ZFPs (i.e., >>106) from a total of 768 oligonucleotides. The invention also is directed to a method of prepg. artificial transcription factors.

L3 ANSWER 4 OF 12 CA COPYRIGHT 2003 ACS on STN
AB The invention concerns polypeptides with novel DNA binding specificities, constructed from combinations of zinc fingers, and methods for their prepn. and use. The present invention recognizes the potential importance of designer zinc finger peptides in therapeutic and transgenic applications in animals and plants. Furthermore the present invention acknowledges that the safety of such applications is of primary importance. The present invention provides the isolation of natural zinc finger modules, from genomes and the construction of nonnatural combinations of such zinc finger modules, to create multi-finger domains, and to provide and det. novel nucleic acid binding specificities. Such a procedure will allow the identification of the novel zinc finger domains that bind any desired nucleic acid sequence. The present invention thus greatly enhances the possibilities for the use of zinc finger transcription factors for in vivo applications, such as gene therapy and transgenic animals.

L3 ANSWER 5 OF 12 CA COPYRIGHT 2003 ACS on STN
AB There is considerable interest in mols. that bind to telomeric DNA sequences and G-quadruplexes with specificity. Such mols. would be useful to test hypotheses for telomere length regulation, and may have therapeutic potential. The versatility and modular nature of the zinc finger motif makes it an ideal candidate for engineering G-quadruplex-binding proteins. Phage display technol. has previously been widely used to screen libraries of zinc fingers for binding to novel duplex DNA sequences. In this study, a three-finger library has been screened for clones that bind to an oligonucleotide contg. the human telomeric repeat sequence folded in the G-quadruplex conformation. The selected clones show a strong amino acid consensus, suggesting analogous modes of binding. Binding was found to be both sequence dependent and structure specific. This is the first example of an engineered **protein** that binds to G-quadruplex DNA, and represents a new type of binding interaction for a **zinc finger protein**.

L3 ANSWER 6 OF 12 CA COPYRIGHT 2003 ACS on STN
AB A method is described for selecting DNA-binding proteins that recognize described sequences. The protocol involves gradually extending a new **zinc finger protein** across the desired 9- or 10-base pair target site, adding and optimizing one finger at a time. This procedure was tested with a TATA box, a p53 binding site, and a nuclear receptor element, and proteins were obtained that bind with nanomolar dissocn. consts. and discriminate effectively (greater than

20,000-fold) against nonspecific DNA. This strategy may provide important information about **protein**-DNA recognition as well as powerful tools for biomedical research.

L3 ANSWER 7 OF 12 CA COPYRIGHT 2003 ACS on STN
AB Libraries of the zinc finger DNA binding **protein**, Zif268, were constructed and selected for affinity and specificity toward DNA targets using the phage display technique. Mutant proteins were purified to homogeneity and were characterized for their ability to interact with their DNA targets using a real-time biomol. interaction assay (BIA). One mutant **protein**, C7, bound the Zif268 consensus binding sequence with a 13-fold increase in affinity as compared to the wild-type Zif268 **protein**. Mutant proteins with moderate affinity for new DNA targets within a consensus sequence of HIV-1 were also obtained. Surface plasmon resonance based BIA has provided invaluable kinetic information which offers insights into the mechanism of **protein**-DNA interactions.

L3 ANSWER 8 OF 12 CA COPYRIGHT 2003 ACS on STN
AB In the preceding paper [Choo, Y. & Klug, A. (1994) Proc. Natl. Acad. Sci. USA 91, 11163-11167], the authors showed how selections from a library of zinc fingers displayed on phage yielded fingers able to bind to a no. of DNA triplets. Here, they describe a technique to deal efficiently with the converse problem-namely, the selection of a DNA binding site for a given zinc finger. This is done by screening against libraries of DNA triplet binding sites randomized in two positions but having one base fixed in the third position. The technique is applied here to det. the specificity of fingers previously selected by phage display. Some of these fingers are able to specify a unique base in each position of the cognate triplet. This is further illustrated by examples of fingers which can discriminate between closely related triplets as measured by their resp. equil. dissocn. consts. Comparing the amino acid sequences of fingers which specify a particular base in a triplet, the authors infer that in most instances, sequence-specific binding of zinc fingers to DNA can be achieved by using a small set of amino acid-nucleotide base contacts amenable to a code.

L3 ANSWER 9 OF 12 CA COPYRIGHT 2003 ACS on STN
AB The screening of **combinatorial libraries** is becoming a powerful method for identifying or refining the structures of ligands for binding proteins, enzymes, and other receptors. An oligonucleotide library search procedure is described in which the identity of each member is encoded in the length of oligonucleotides. This encoding scheme allows binding-site preferences to be evaluated via DNA length detn. by denaturing gel electrophoresis. This method was applied to det. the binding-site preferences for 18 Cys2His2 zinc finger domains as the central domain within a fixed context of flanking zinc fingers. An advantage of the method is that the relative affinities of all members of the library can be estd. in addn. to simply detg. the sequence of the optimal or consensus ligand. The zinc finger domain specificities detd. will be useful for modular **zinc finger protein** design.

L3 ANSWER 10 OF 12 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
AB The ability to selectively regulate the expression of genes implicated in cancer or other diseases could have important ramifications for both basic research and for therapy. Using peptide **combinatorial libraries** expressed in yeast, we have screened for novel zinc finger proteins that selectively bind to an overlapping EGR1/SP1/WT1 regulatory site in the promoter of the MDR1 multidrug resistance gene. The novel proteins were only moderately effective in blocking transcription by simple masking of the target site. However, when coupled to mammalian transactivator or repressor domains, they could selectively modulate the expression of reporter genes having promoters containing the MDR1 target site. Moreover, they could also regulate transcription of the chromosomal

mol., methods for calcg. the dissocn. const. of a ligand compd. which binds to a 13C-enriched target mol., and methods employed in the detn. of the specific amino acids in a 13C-enriched target mol. affected by the binding of a ligand, as well as compds. identified by these screening methods, are provided herewith.

L7 ANSWER 4 OF 8 CA COPYRIGHT 2003 ACS on STN
TI Production by site-specific recombination of recombinant vectors for production of antibodies using display on secreted replicable genetic display packages
IN Griffiths, Andrew David; Williams, Samuel Cameron; Waterhouse, Peter Michael; Nissim, Ahuva; Winter, Gregory Paul; Johnson, Kevin Stuart; Smith, Andrew John Hammond
SO U.S., 184 pp., Cont.-in-part of U.S. Ser. No. 307,619.
CODEN: USXXAM
PY 1999
1993
1996
1995
1995
1999
1998
2000
2001
2002
AB Methods, recombinant host cells and kits are disclosed for the prodn. of members of specific binding pairs (sbp), e.g. antibodies, using display on the surface of secreted replicable genetic display packages (rgdps), e.g. filamentous phage. To produce a library of great diversity recombination occurs between first and second vectors comprising nucleic acid encoding first and second polypeptide chains of sbp members resp., thereby producing recombinant vectors each encoding both a first and a second polypeptide chain component of a sbp member. The recombination may take place in vitro or intracellularly and may be site-specific, e.g. involving use of the loxP sequence and mutants thereof. Recombination may take place after prior screening or selecting for rgdps displaying sbp members which bind complementary sbp member of interest. Thus, a highly diverse combinatorial repertoire was constructed in Escherichia coli using Ig V domains as building blocks. First, highly diverse repertoires of H and L chains were created entirely in vitro from a bank of human V domain segments and then, by recombination of the repertoires in E. coli, generated a large (close to 6.5 X 1010) synthetic repertoire of Fab fragments displayed on filamentous phage. The process involved infecting, with an "acceptor" L chain repertoire (on fd phage), E. coli harboring a "donor" H chain repertoire (on a plasmid). The two chains were then combined on the same (fd phage) replicon within the bacterium by Cre catalyzed recombination at loxP sites. From the resulting repertoire Fab fragments were isolated which bound to a range of different antigens and haptens with binding affinities comparable to those of antibodies from a secondary immune response in mice (up to 4 nM).

L7 ANSWER 5 OF 8 CA COPYRIGHT 2003 ACS on STN
TI Combinatorics assisted large throughput screening of oligonucleotide libraries for drug activity
IN Paul, Dieter; Stadler, Herbert
SO Ger. Offen., 6 pp.
CODEN: GWXXBX
PY 1999
AB The invention concerns a math. method for increasing the throughput when isolating an x-mer oligonucleotide from a library that contains all 4x-mers by dividing the library into **256** sub-libraries with predetd. sequences in the x, x-1, x-2, x-3 positions; each of the sub-libraries is screened with the target substance; the sublibrary contg. the binding sequence is again divided in **256** sublibraries with defined sequences in the x-4, x-5, x-6, x-7 positions; these sublibraries

are screened again with the target substance; these procedure is repeated until the total sequence of the binding oligonucleotide is found. Oligonucleotides are produced in solid phase combinatorial synthesis; target substances, e.g. proteins involved in diseases are immobilized onto biochips. Biochips are silicon layers with waveguides; the immobilized proteins are contacted with a soln. of fluorescent labeled oligonucleotides; upon binding with the target mol., the fluorescent signal is detected. After amplification of the identified oligonucleotide, the drug candidate is used in a second screening, e.g. with tissue cultures or disease model animals.

L7 ANSWER 6 OF 8 CA COPYRIGHT 2003 ACS on STN
TI Phenotypic assays of for modulators of cyclin/cyclin-dependent kinase function
IN Bitter, Grant A.
SO PCT Int. Appl., 94 pp.
CODEN: PIXXD2
PY 1998
1998
2000
AB A method of screening for a compd. that affects mammalian cell cycle regulatory proteins comprises (A) administering a compd. to a cell line and (b) analyzing expression of the reporter gene in the cell line, thereby detg. whether the compd. affects normal regulation. The cell line comprises genetic information comprising (1) a reporter gene operably linked to a gene expression control sequence and promoter and (2) a hybrid gene comprising a first coding region from a gene native to the cell line and a second coding region from a second gene. The upstream activation sequence comprises a DNA region that binds to a transcription control factor that is regulated through phosphorylation by a cyclin/CDK phosphorylation system. The first gene encodes a gene product that affects phosphorylation by the cyclin/CDK phosphorylation system, and the second gene is mammalian and is homologous to the native gene; the hybrid gene provides a gene product effective to permit normal cyclin/CDK regulation of the transcription control factor. Specific cell lines and methods are also part of the present invention. Thus, a hybrid **protein** is constructed comprising a first coding region for amino acids 155-302 of Saccharomyces cerevisiae PHO85, and the second target gene encodes amino acids 1-151 of human CDK2. In another embodiment, the hybrid gene encodes amino acids 155-251 from PHO85 linked to a second coding region encoding amino acids 1-151 from human CDK2, and a third coding region for amino acids **256**-298 of CDK2. Two reporter genes were evaluated for suitability to allow pos. selections for cyclin/CDK inhibitor: the Escherichia coli tn5 neo gene product that confers resistance to the antibiotic G418, and the yeast LEU2 gene involved in leucine biosynthesis. The yeast cell line may have disruptions in genes PDR1, PDR5, SN22, YOR1, PDR3 which impairs their ability to transport certain compds. out of the cell. The screen distinguishes specific cyclin/CDK inhibitors from general cytotoxic compds.

L7 ANSWER 7 OF 8 CA COPYRIGHT 2003 ACS on STN
TI Screening Derivatized Peptide Libraries for Tight Binding Inhibitors to Carbonic Anhydrase II by Electrospray Ionization-Mass Spectrometry
AU Gao, Jinming; Cheng, Xueheng; Chen, Ruidan; Sigal, George B.; Bruce, James E.; Schwartz, Brenda L.; Hofstadler, Steven A.; Anderson, Gordon A.; Smith, Richard D.; Whitesides, George M.
SO Journal of Medicinal Chemistry (1996), 39(10), 1949-55
CODEN: JMCMAR; ISSN: 0022-2623
PY 1996
AB This paper describes the use of electrospray ionization-mass spectrometry (ESI-MS) to screen 2 libraries of sol. compds. to search for tight binding inhibitors for carbonic anhydrase II (EC 4.2.1.1). The 2 libraries, H2NO2SC6H4C(O)NH-AA1-AA2-C(O)NHCH2CH2CO2H, where AA1 and AA2 are L-amino acids (library size: 289 compds.) or D-amino acids (**256**

compds.), were constructed by attaching tripeptides to the carboxyl group of 4-carboxybenzenesulfonamide. Screening of both libraries yielded, as the tightest binding inhibitor, the compd. (AA1 = AA2 = L-Leu; binding const. Kb = 1.4 .times. 108 M-1). The ability of ESI-MS to est. simultaneously the relative binding affinities of a **protein** to sol. ligands in a library, if general, should be useful in drug development.

L7 ANSWER 8 OF 8 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
TI Stepwise in vitro affinity maturation of Vitaxin, an alphavbeta3-specific humanized mAb.
AU Wu, Herren; Beuerlein, Gregory; Nie, Ying; Smith, Heidi; Lee, Bruce A.; Hensler, Mary; Huse, William D.; Watkins, Jeffry D. (1)
SO Proceedings of the National Academy of Sciences of the United States of America, (May 26, 1998) Vol. 95, No. 11, pp. 6037-6042.
ISSN: 0027-8424.
PY 1998
AB A **protein** engineering strategy based on efficient and focused mutagenesis implemented by codon-based mutagenesis was developed. Vitaxin, a humanized version of the antiangiogenic antibody LM609 directed against a conformational epitope of the alphavbeta3 integrin complex, was used as a model system. Specifically, focused mutagenesis was used in a stepwise fashion to rapidly improve the affinity of the antigen binding fragment by greater than 90-fold. In the complete absence of structural information about the Vitaxinalphavbeta3 interaction, phage-expressed antibody libraries for all six Ig heavy and light chain complementarity-determining regions were expressed and screened by a quantitative assay to identify variants with improved binding to alphavbeta3. The Vitaxin variants in these libraries each contained a single mutation, and all 20 amino acids were introduced at each complementarity-determining region residue, resulting in the expression of 2,336 unique clones. Multiple clones displaying 2- to 13-fold improved affinity were identified. Subsequent expression and screening of a library of **256** combinatorial variants of the optimal mutations identified from the primary libraries resulted in the identification of multiple clones displaying greater than 50-fold enhanced affinity. These variants inhibited ligand binding to receptor more potently as demonstrated by inhibition of cell adhesion and ligand competition assays. Because of the limited mutagenesis and combinatorial approach, Vitaxin variants with enhanced affinity were identified rapidly and required the synthesis of only 2,592 unique variants. The use of such small focused libraries obviates the need for phage affinity selection approaches typically used, permitting the use of functional assays and the engineering of proteins expressed in mammalian cell culture.

=> d his

(FILE 'HOME' ENTERED AT 08:59:46 ON 11 AUG 2003)

FILE 'CA, BIOSIS, MEDLINE' ENTERED AT 08:59:58 ON 11 AUG 2003
L1 9924 S COMBINATORIAL(3W)LIBRA?
L2 2662 S L1 AND (ATF OR ARTIFICIAL(2W)TRANSCRIPTION(2W)FACTOR OR PROTE
L3 12 S L2 AND (ZFP OR ZINC FINGER PROTEIN)
L4 2650 S L2 NOT L3
L5 0 S L4 AND 256(3W)BP
L6 0 S L4 AND 256(6W)FOUR(2W)(BP OR BASE(2W)PAIR)
L7 8 S L4 AND 256

=> log y

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	80.63	80.84

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE	TOTAL

	ENTRY	SESSION
CA SUBSCRIBER PRICE	-9.92	-9.92

STN INTERNATIONAL LOGOFF AT 09:04:05 ON 11 AUG 2003

MDR1 gene. Thus, in K562 cells, 12-O-tetradecanoylphorbol-13-acetate-inducible expression of P-glycoprotein, the product of MDR1 gene, was strongly and selectively inhibited by the presence of a repressor **protein** targeted to the MDR1 promoter. These studies potentially provide a novel alternative approach to the control of multidrug resistance. They also provide important insights into strategies for developing selective regulators of gene expression.

L3 ANSWER 11 OF 12 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
AB The screening of **combinatorial libraries** is becoming a powerful method for identifying or refining the structures of ligands for binding proteins, enzymes, and other receptors. We describe an oligonucleotide library search procedure In which the identity of each member is encoded in the length of oligonucleotides. This encoding scheme BETA-ows bindIng-site preferences to be evaluated via DNA length determination by denaturing gel electrophoresis. We have applied this method to determine the binding-site preferences for 18 Cys-2His-2 zinc finger domains as the central domain within a fixed context of flanking zinc fingers. An advantage of the method is that the relative affinities of all members of the library can be estimated in addition to simply determining the sequence of the optimal or consensus ligand. The zinc finger domain specificities determined will be useful for modular **zinc finger protein** design.

L3 ANSWER 12 OF 12 MEDLINE on STN
AB The screening of **combinatorial libraries** is becoming a powerful method for identifying or refining the structures of ligands for binding proteins, enzymes, and other receptors. We describe an oligonucleotide library search procedure in which the identity of each member is encoded in the length of oligonucleotides. This encoding scheme allows binding-site preferences to be evaluated via DNA length determination by denaturing gel electrophoresis. We have applied this method to determine the binding-site preferences for 18 Cys2His2 zinc finger domains as the central domain within a fixed context of flanking zinc fingers. An advantage of the method is that the relative affinities of all members of the library can be estimated in addition to simply determining the sequence of the optimal or consensus ligand. The zinc finger domain specificities determined will be useful for modular **zinc finger protein** design.

```
=> d his

     (FILE 'HOME' ENTERED AT 08:59:46 ON 11 AUG 2003)

     FILE 'CA, BIOSIS, MEDLINE' ENTERED AT 08:59:58 ON 11 AUG 2003
L1          9924 S COMBINATORIAL(3W)LIBRA?
L2          2662 S L1 AND (ATF OR ARTIFICIAL(2W)TRANSCRIPTION(2W)FACTOR OR PROTE
L3            12 S L2 AND (ZFP OR ZINC FINGER PROTEIN)

=> s l2 not l3
L4          2650 L2 NOT L3

=> s l4 and 256(3w)bp
L5             0 L4 AND 256(3W) BP

=> s l4 and 256(6w)four(2w)(bp or base(2w)pair)
L6             0 L4 AND 256(6W) FOUR(2W)(BP OR BASE(2W) PAIR)

=> s l4 and 256
L7             8 L4 AND 256

=> d l7 1-8 ti au so py ab

L7   ANSWER 1 OF 8  CA  COPYRIGHT 2003 ACS on STN
```

TI Human olfactory receptors and genes encoding same, methods for representing and modulating olfactory perception, and biosensors of chemical sensants
IN Zozulya, Sergey; Stryer, Lubert
SO PCT Int. Appl., 182 pp.
CODEN: PIXXD2
PY 2001
2003
2002
2002
AB Newly identified olfactory G **protein**-coupled receptors (ORs), and the genes and cDNA encoding said receptors are described. Specifically, **256** human G **protein**-coupled receptors active in olfactory signaling, and the genes and cDNA encoding the same, are described, along with methods for isolating such genes and for isolating and expressing such receptors. The use of such products as a biosensor or a components thereof to detect, identify, measure, or otherwise process the event of binding between the receptor and its cognate ligand (i.e., chem. sensant) is also described. All these receptor genes were initially detected by computer DNA sequence anal. of genomic clones from the High Throughput Genome Sequence database of GenBank. Primer pairs are used for amplification of olfactory receptor transmembrane domains II through VII. Methods for representing olfactory perception of a particular odorant in a mammal are also described, as are methods for generating novel mols. or combinations of mols. that elicit a predetd. odor perception in a mammal, and methods for simulating one or more odors. Further, methods for stimulating or blocking odor perception in a mammal are also disclosed. The invention has application, for example, in the design and formulation of odorant and tastant compns.

L7 ANSWER 2 OF 8 CA COPYRIGHT 2003 ACS on STN
TI Human olfactory receptors and genes encoding same
IN Zozulya, Sergey
SO PCT Int. Appl., 319 pp.
CODEN: PIXXD2
PY 2001
2003
2001
2003
AB Newly identified olfactory G **protein**-coupled receptors (ORs), and the genes and cDNA encoding said receptors are described. Specifically, **256** human G **protein**-coupled receptors active in olfactory signaling, and the genes and cDNA encoding the same, are described, along with methods for isolating such genes and for isolating and expressing such receptors. All these receptor genes were initially detected by computer DNA sequence anal. of genomic clones from the High Throughput Genome Sequence database of GenBank. Primer pairs are used for amplification of olfactory receptor transmembrane domains II through VII. Methods for representing olfactory perception of a particular odorant in a mammal are also described, as are methods for generating novel mols. or combinations of mols. that elicit a predetd. odor perception in a mammal, and methods for simulating one or more odors. Further, methods for stimulating or blocking odor perception in a mammal are also disclosed.

L7 ANSWER 3 OF 8 CA COPYRIGHT 2003 ACS on STN
TI Use of 13C-NMR to detect binding
IN Fesik, Stephen W.; Hajduk, Philip J.
SO PCT Int. Appl., 52 pp.
CODEN: PIXXD2
PY 2000
2001
2002
AB Methods of detecting binding of a putative ligand to a 13C-enriched target mol., methods of screening for compds. which bind to a 13C-enriched target

```
Connecting via Winsock to STN


Welcome to STN International!  Enter x:x

LOGINID:sssptau183tw

PASSWORD:
TERMINAL (ENTER 1, 2, 3, OR ?):2


* * * * * * * * * *   Welcome to STN International   * * * * * * * * * *

 NEWS  1           Web Page URLs for STN Seminar Schedule - N. America
 NEWS  2           "Ask CAS" for self-help around the clock
 NEWS  3  Feb 24   PCTGEN now available on STN
 NEWS  4  Feb 24   TEMA now available on STN
 NEWS  5  Feb 26   NTIS now allows simultaneous left and right truncation
 NEWS  6  Feb 26   PCTFULL now contains images
 NEWS  7  Mar 04   SDI PACKAGE for monthly delivery of multifile SDI results
 NEWS  8  Mar 24   PATDPAFULL now available on STN
 NEWS  9  Mar 24   Additional information for trade-named substances without
                   structures available in REGISTRY
 NEWS 10  Apr 11   Display formats in DGENE enhanced
 NEWS 11  Apr 14   MEDLINE Reload
 NEWS 12  Apr 17   Polymer searching in REGISTRY enhanced
 NEWS 13  Jun 13   Indexing from 1947 to 1956 added to records in CA/CAPLUS
 NEWS 14  Apr 21   New current-awareness alert (SDI) frequency in
                   WPIDS/WPINDEX/WPIX
 NEWS 15  Apr 28   RDISCLOSURE now available on STN
 NEWS 16  May 05   Pharmacokinetic information and systematic chemical names
                   added to PHAR
 NEWS 17  May 15   MEDLINE file segment of TOXCENTER reloaded
 NEWS 18  May 15   Supporter information for ENCOMPPAT and ENCOMPLIT updated
 NEWS 19  May 19   Simultaneous left and right truncation added to WSCA
 NEWS 20  May 19   RAPRA enhanced with new search field, simultaneous left and
                   right truncation
 NEWS 21  Jun 06   Simultaneous left and right truncation added to CBNB
 NEWS 22  Jun 06   PASCAL enhanced with additional data
 NEWS 23  Jun 20   2003 edition of the FSTA Thesaurus is now available
 NEWS 24  Jun 25   HSDB has been reloaded
 NEWS 25  Jul 16   Data from 1960-1976 added to RDISCLOSURE
 NEWS 26  Jul 21   Identification of STN records implemented
 NEWS 27  Jul 21   Polymer class term count added to REGISTRY
 NEWS 28  Jul 22   INPADOC: Basic index (/BI) enhanced; Simultaneous Left and
                   Right Truncation available
 NEWS 29  AUG 05   New pricing for EUROPATFULL and PCTFULL effective
                   August 1, 2003

 NEWS EXPRESS  April 4 CURRENT WINDOWS VERSION IS V6.01a, CURRENT
               MACINTOSH VERSION IS V6.0b(ENG) AND V6.0Jb(JP),
               AND CURRENT DISCOVER FILE IS DATED 01 APRIL 2003
 NEWS HOURS    STN Operating Hours Plus Help Desk Availability
 NEWS INTER    General Internet Information
 NEWS LOGIN    Welcome Banner and News Items
 NEWS PHONE    Direct Dial and Telecommunication Network Access to STN
 NEWS WWW      CAS World Wide Web Site (general information)

Enter NEWS followed by the item number or name to see news on that
specific topic.

  All use of STN is subject to the provisions of the STN Customer
```

```
  agreement.  Please note that this agreement limits use to scientific
  research.  Use for software development or design or implementation
  of commercial gateways or other similar uses is prohibited and may
  result in loss of user privileges and other penalties.

  * * * * * * * * * * * * * STN  Columbus  * * * * * * * * * * * * * * * *

FILE 'HOME' ENTERED AT 08:59:46 ON 11 AUG 2003

=> file ca biosis medline
COST IN U.S. DOLLARS                                    SINCE FILE      TOTAL
                                                           ENTRY    SESSION
FULL ESTIMATED COST                                         0.21       0.21

FILE 'CA' ENTERED AT 08:59:58 ON 11 AUG 2003
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
COPYRIGHT (C) 2003 AMERICAN CHEMICAL SOCIETY (ACS)

FILE 'BIOSIS' ENTERED AT 08:59:58 ON 11 AUG 2003
COPYRIGHT (C) 2003 BIOLOGICAL ABSTRACTS INC.(R)

FILE 'MEDLINE' ENTERED AT 08:59:58 ON 11 AUG 2003

=> s combinatorial(3w)libra?
L1         9924 COMBINATORIAL(3W) LIBRA?

=> s l1 and (ATF or artificial(2w)transcription(2w)factor or protein)
L2         2662 L1 AND (ATF OR ARTIFICIAL(2W) TRANSCRIPTION(2W) FACTOR OR PROTEI
                N)

=> s l2 and (zfp or zinc finger protein)
L3           12 L2 AND (ZFP OR ZINC FINGER PROTEIN)

=> d l3 1-12

L3   ANSWER 1 OF 12  CA  COPYRIGHT 2003 ACS on STN
AN   138:380506  CA
TI   Genes that are differentially expressed during erythropoiesis and their
     diagnostic and therapeutic uses
IN   Brissette, William H.; Neote, Kuldeep S.; Zagouras, Panayiotis; Zenke,
     Martin; Lemke, Britt; Hacker, Christine
PA   Pfizer Products Inc., USA; Max-Delbruck-Centre for Molecular Medicine
SO   PCT Int. Appl., 285 pp.
     CODEN: PIXXD2
DT   Patent
LA   English
FAN.CNT 2
     PATENT NO.         KIND  DATE           APPLICATION NO.  DATE
     ---------------    ----  --------       ---------------  --------
PI   WO 2003038130      A2    20030508       WO 2002-XA34888  20021031
         W:  AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
             CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,
             GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
             LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH,
             PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ,
             UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU,
             TJ, TM
         RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG,
             CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL,
             PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR,
             NE, SN, TD, TG
     WO 2003038130      A2    20030508       WO 2002-US34888  20021031
         W:  AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
             CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,
```

GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH,
PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ,
UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU,
TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG,
CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL,
PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR,
NE, SN, TD, TG

PRAI US 2001-335048P P 20011031
US 2001-335183P P 20011102
WO 2002-US34888 A 20021031

L3 ANSWER 2 OF 12 CA COPYRIGHT 2003 ACS on STN
AN 138:380471 CA
TI Genes that are differentially expressed during erythropoiesis and their diagnostic and therapeutic uses
IN Brissette, William H.; Neote, Kuldeep S.; Zagouras, Panayiotis; Zenke, Martin; Lemke, Britt; Hacker, Christine
PA Pfizer Products Inc., USA; Max-Delbruck-Centre for Molecular Medicine
SO PCT Int. Appl., 285 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 2

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2003038130	A2	20030508	WO 2002-US34888	20021031

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

WO 2003038130	A2	20030508	WO 2002-XA34888	20021031

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRAI US 2001-335048P P 20011031
US 2001-335183P P 20011102
WO 2002-US34888 A 20021031

L3 ANSWER 3 OF 12 CA COPYRIGHT 2003 ACS on STN
AN 138:350273 CA
TI Rules for design of sequence-specific zinc finger peptides and the design of novel DNA binding proteins for regulation of genetic processes
IN Sera, Takashi
PA USA
SO U.S. Pat. Appl. Publ., 72 pp., Cont.-in-part of U.S. Ser. No. 911,261.
CODEN: USXXCO
DT Patent
LA English

FAN.CNT 2

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 2003082561	A1	20030501	US 2002-57408	20020123
	US 2003134350	A1	20030717	US 2001-911261	20010723
	WO 2003062455	A2	20030731	WO 2003-US2358	20030123

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRAI	US 2000-220060P	P	20000721
	US 2001-911261	A2	20010723
	US 2002-57408	A	20020123

L3 ANSWER 4 OF 12 CA COPYRIGHT 2003 ACS on STN
AN 138:35762 CA
TI Sequence-specific binding based on designed zinc finger peptides
IN Moore, Michael; Sepp, Armin; Isalan, Mark; Choo, Yen
PA Sangamo Biosciences, Inc, USA
SO PCT Int. Appl., 157 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2002099084	A2	20021212	WO 2002-US22272	20020404

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRAI	GB 2001-8491	A	20010404

L3 ANSWER 5 OF 12 CA COPYRIGHT 2003 ACS on STN
AN 134:189667 CA
TI Selection of Zinc Fingers that Bind Single-Stranded Telomeric DNA in the G-Quadruplex Conformation
AU Isalan, Mark; Patel, Sachin D.; Balasubramanian, Shankar; Choo, Yen
CS Department of Chemistry, University of Cambridge, Cambridge, CB2 1EW, UK
SO Biochemistry (2001), 40(3), 830-836
CODEN: BICHAW; ISSN: 0006-2960
PB American Chemical Society
DT Journal
LA English
RE.CNT 40 THERE ARE 40 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L3 ANSWER 6 OF 12 CA COPYRIGHT 2003 ACS on STN
AN 126:197076 CA
TI A general strategy for selecting high-affinity zinc finger proteins for diverse DNA target sites
AU Greisman, Harvey A.; Pabo, Carl O.
CS Howard Hughes Med. Inst. Dep. Biol., Massachusetts Inst. Technol.,